Amendments to the Specification:

Please replace paragraph **[0016]** beginning at page 4, line 14, with the following:

--**[0016]** In a second embodiment, the pathology, disease or disorder is a cancer of the oral cavity and/or of oropharynx, the bodily fluid is blood serum and the gene is selected from IL6 (interleukin 6), H3F3A, TPT1 (Tumor protein ~~trnslationally~~ translationally controlled 1), FTH1 (Ferritin heavy polypeptide 1), NCOA4 (Nuclear receptor coactivator 4) and ARCR (Ras homolog gene family, member A).--

Please replace paragraph **[00115]** beginning at page 23, line 13, with the following:

--**[00115]** The quality of isolated RNA was examined by RT-PCR for three house-keeping gene transcripts: glyceraldehyde-3-phosphate dehydrogenase (GAPDH), actin-β (ACTB) and ribosomal protein S9 (RPS9). Primers were designed using PR!MER3 software (http://www.genome.wi.mit.edu) and were synthesized commercially (Fisher Scientific, Tustin, CA, USA) as follows: the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 1 and SEQ ID NO: 2 for GAPDH; the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 3 and SEQ ID NO: 4 for ACTB; the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 5 and SEQ ID NO: 6 for RPS9. The quantity of RNA was estimated using Ribogreen® RNA Quantitation Kit (Molecular Probes, Eugene, OR, USA). The results are shown in Figure 1B, wherein GAPDH *(B1)*, RPS9 *(B2)* and ACTB *(B3)* were detected consistently in all 10 cases tested, demonstrating that all 10 saliva samples contain mRNAs that encode for house keeping genes: GAPDH, ACTB and RPS9.--

Please replace paragraph **[00117]** beginning at page 24, line 2, with the following:

--**[00117]** Isolated RNA was then subjected to linear amplification according to published method from our laboratory (Ohyama *et al.*, 2000). In brief, reverse transcription using T7-oligo-$(dT)_{24}$ (SEQ ID NO:53) as the primer was performed to synthesize the first strand cDNA. The first round of *in vitro* transcription (IVT) was carried out using T7 RNA polymerase (Ambion Inc., Austin, TX, USA). The BioArray™ High Yield RNA Transcript Labeling System (Enzo Life Sciences, Farmingdale, NY, USA) was used for the second round IVT to biotinylate the cRNA product; the labeled cRNA was purified using GeneChip® Sample Cleanup Module (Affymetrix, Santa Clara, CA, USA).--

Please replace paragraph **[00130]** beginning at page 28, line 8, with the following:

--**[00130]** Q-PCR was performed using iCycler™ thermal Cycler (Bio-Rad, Hercules, CA, USA). A 2 μL aliquot of the isolated salivary RNA (without amplification) was reverse transcribed into cDNA using MuLV Reverse Transcriptase (Applied Biosystems, Foster City, CA, USA). The resulting cDNA (3 μL) was used for PCR amplification using iQ SYBR Green Supermix (Bio-Rad, Hercules, CA, USA). The primers were synthesized by Sigma-Genosys (Woodlands, TX, USA) as follows: the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 7 and SEQ ID NO: 8 for interleukin 1, beta (IL1B); the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 9 [[nd]] and SEQ ID NO: 10 for stratifin (SFN); the primers having the sequence reported in the attached sequence listing as SEQ ID NO: 11 and SEQ ID NO: 12 for tubulin, alpha, ubiquitous (K-ALPHA-1). All reactions were performed in triplicate with conditions customized for the specific PCR products. The initial amount of cDNA of a particular template was extrapolated from a standard curve using the LightCycler software 3.0 (Bio-Rad, Hercules, CA, USA). The detailed procedure for quantification by standard curve has been previously described (Ginzinger, 2002).--

Please replace paragraph **[00131]** beginning at page 28, line 25, with the following:

--**[00131]** Q-PCR results showed that mRNA of IL1B, SFN and K-ALPHA-1 were detectable in all 10 original, unamplified, cell-free saliva. The relative amounts (in copy number) of these transcripts (n=10) are: ~~8.68 x 103 ± 4.15 x 103~~ $8.68 \times 10^3 \pm 4.15 \times 10^3$ for IL1B; ~~1.29 x 105 ± 1.08 x 105~~ $1.29 \times 10^5 \pm 1.08 \times 10^5$ for SFN; and ~~4.71 x 106 ± 8.37 x 105~~ $4.71 \times 10^6 \pm 8.37 \times 10^5$ for K-ALPHA-1. The relative RNA expression levels of these genes measured by Q-PCR were similar to those measured by the microarrays (data not shown).--

Please replace paragraph **[00194]** beginning at page 44, line 22, with the following:

--**[00194]** Ten significant up-regulated genes: H3F3A, TPT1, FTH1, NCOA4, ARCR, THSMB (Thymosin beta 10), PRKCB1 (Protein Kinase C, beta 1), FTL1 (Ferritin Light polypeptide), COX4I1 (Cytochrome c oxidase subunit IV isoform 1) and SERP1 (~~srtress~~ stress associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4) were selected based on their reported cancer-association as shown in Table 6, reporting ten genes selected for qPCR validation.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 11, at the end of the application.